

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/559,431
Source: IFWO
Date Processed by STIC: 12/20/2005

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/559, 431

CRF Edit Date: 12/20/2005
Edited by: D/A

___ **Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line**

___ **Corrected the SEQ ID NO. Sequence numbers edited were:**

___ **Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:**

/ Deleted: / **invalid beginning/end-of-file text ;** ___ **page numbers**

___ **Inserted mandatory headings/numeric identifiers, specifically:**

___ **Moved responses to same line as heading/numeric identifier, specifically:**

___ **Other:**



IFWP

RAW SEQUENCE LISTING

DATE: 12/20/2005

PATENT APPLICATION: US/10/559,431

TIME: 13:16:57

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\12202005\J559431.raw

4 <110> APPLICANT: BIOMERIEUX
 5 INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
 7 <120> TITLE OF INVENTION: Composition comprising the polyprotein NS3/NS4 and the
 polypeptide NS5b
 8 of HCV, expression vectors including the corresponding nucleic sequences and
 9 their therapeutic use
 11 <130> FILE REFERENCE: ADENOVIR
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/559,431
 C--> 13 <141> CURRENT FILING DATE: 2005-12-05
 13 <160> NUMBER OF SEQ ID NOS: 27
 15 <170> SOFTWARE: PatentIn version 3.1
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 2844
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Artificial sequence
 22 <220> FEATURE:
 23 <223> OTHER INFORMATION: sequence coding for NS3NS4
 25 <220> FEATURE:
 26 <221> NAME/KEY: CDS
 27 <222> LOCATION: (1)..(2844)
 28 <223> OTHER INFORMATION:
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 33 1 5 10 15
 35 tgt atc atc act agc ctc aca ggt cgg gac aag aac cag gtc gat ggg 96
 36 Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Asp Gly
 37 20 25 30
 39 gag gtt cag gtg ctc tcc acc gca acg caa tct ttc ctg gcg acc tgc 144
 40 Glu Val Gln Val Leu Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys
 41 35 40 45
 43 gtc aat ggc gtg tgt tgg acc gtc tac cat ggt gcc ggc tcg aag acc 192
 44 Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr
 45 50 55 60
 47 ctg gcc ggc ccg aag ggt cca atc acc caa atg tac acc aat gta gac 240
 48 Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp
 49 65 70 75 80
 51 cag gac ctc gtc ggc tgg ccg gcg ccc ccc ggg gcg cgc tcc atg aca 288
 52 Gln Asp Leu Val Gly Trp Pro Ala Pro Pro Gly Ala Arg Ser Met Thr
 53 85 90 95
 55 ccg tgc acc tgc ggc agc tcg gac ctt tac ttg gtc acg agg cat gcc 336
 56 Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala
 57 100 105 110
 59 gat gtc att ccg gtg cgc cgg cga ggc gac agc agg ggg agt cta ctc 384

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64 Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu
65      130      135      140
67 ctt tgc cct tcg ggg cac gtt gta ggc atc ttc cgg gct gct gtg tgc      480
68 Leu Cys Pro Ser Gly His Val Val Gly Ile Phe Arg Ala Ala Val Cys
69 145      150      155      160
71 acc cgg ggg gtt gcg aag gcg gtg gac ttc ata ccc gtt gag tct atg      528
72 Thr Arg Gly Val Ala Lys Ala Val Asp Phe Ile Pro Val Glu Ser Met
73      165      170      175
75 gaa act acc atg cgg tct ccg gtc ttc aca gac aac tca tcc cct ccg      576
76 Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro
77      180      185      190
79 gcc gta ccg caa aca ttc caa gtg gca cat tta cac gct ccc act ggc      624
80 Ala Val Pro Gln Thr Phe Gln Val Ala His Leu His Ala Pro Thr Gly
81      195      200      205
83 agc ggc aag agc acc aaa gtg ccg gct gca tat gca gcc caa ggg tac      672
84 Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr
85      210      215      220
87 aag gtg ctc gtc cta aac ccg tcc gtt gct gcc aca ttg ggc ttt gga      720
88 Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly
89 225      230      235      240
91 gcg tat atg tcc aag gca cat ggc atc gag cct aac atc aga act ggg      768
92 Ala Tyr Met Ser Lys Ala His Gly Ile Glu Pro Asn Ile Arg Thr Gly
93      245      250      255
95 gta agg acc atc acc acg ggc ggc ccc atc acg tac tcc acc tat ggc      816
96 Val Arg Thr Ile Thr Thr Gly Gly Pro Ile Thr Tyr Ser Thr Tyr Gly
97      260      265      270
99 aag ttc ctt gcc gac ggt gga tgc tcc ggg ggc gcc tat gac atc ata      864
100 Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile
101      275      280      285
103 ata tgt gac gaa tgc cac tca act gac tgg aca acc atc ttg ggc atc      912
104 Ile Cys Asp Glu Cys His Ser Thr Asp Trp Thr Thr Ile Leu Gly Ile
105      290      295      300
107 ggc aca gtc ctg gat cag gca gag acg gct gga gcg cgg ctc gtc gtg      960
108 Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val
109 305      310      315      320
111 ctc gcc acc gcc acg cct ccg gga tcg atc acc gtg cca cac ccc aac      1008
112 Leu Ala Thr Ala Thr Pro Pro Gly Ser Ile Thr Val Pro His Pro Asn
113      325      330      335
115 atc gag gaa gtg gcc ctg tcc aac act ggg gag att ccc ttc tat ggc      1056
116 Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe Tyr Gly
117      340      345      350
119 aaa gcc atc ccc att gag gcc atc aag ggg gga agg cat ctc atc ttc      1104
120 Lys Ala Ile Pro Ile Glu Ala Ile Lys Gly Gly Arg His Leu Ile Phe
121      355      360      365
123 tgc cat tcc aag aag aag tgt gac gag ctc gcc gca aag ctg aca ggc      1152
124 Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Thr Gly

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125	370	375	380	
127	ctc gga ctc aat gct gta gcg tat tac cgg ggt ctc gat gtg tcc gtc	1200		
128	Leu Gly Leu Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val			
129	385	390	395	400
131	ata ccg act agc gga gac gtc gtt gtc gtg gca aca gac gct cta atg	1248		
132	Ile Pro Thr Ser Gly Asp Val Val Val Val Ala Thr Asp Ala Leu Met			
133		405	410	415
135	acg ggc ttt acc ggc gac ttt gac tca gtg atc gac tgc aac aca tgt	1296		
136	Thr Gly Phe Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys			
137		420	425	430
139	gtc acc cag aca gtc gat ttc agc ttg gat ccc acc ttc acc att gag	1344		
140	Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu			
141		435	440	445
143	acg aca acc gtg ccc caa gac gcg gtg tcg cgc tcg cag cgg cga ggt	1392		
144	Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly			
145		450	455	460
147	agg act ggc agg ggc agg agt ggc atc tac agg ttt gtg act cca gga	1440		
148	Arg Thr Gly Arg Gly Arg Ser Gly Ile Tyr Arg Phe Val Thr Pro Gly			
149	465	470	475	480
151	gaa cgg ccc tca ggc atg ttc gac tcc tcg gtc ctg tgt gag tgc tat	1488		
152	Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr			
153		485	490	495
155	gac gca ggc tgc gct tgg tat gag ctc acg ccc gct gag act aca gtc	1536		
156	Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Thr Val			
157		500	505	510
159	agg ttg cgg gct tac ctg aat aca cca ggg ttg ccc gtc tgc cag gac	1584		
160	Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys Gln Asp			
161		515	520	525
163	cat ctg gag ttc tgg gaa agc gtc ttc aca ggc ctc acc cac ata gat	1632		
164	His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp			
165		530	535	540
167	gcc cac ttc ctg tcc caa acc aag cag gca gga gac aac ttc ccc tac	1680		
168	Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe Pro Tyr			
169	545	550	555	560
171	ctg gtg gca tac caa gcc acg gtg tgc gcc agg gct cag gct cca cct	1728		
172	Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro			
173		565	570	575
175	cca tcg tgg gat caa atg tgg aag tgt ctc ata cgg ctt aaa cct acg	1776		
176	Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr			
177		580	585	590
179	ctg cac ggg cca aca ccc ctg ctg tat agg cta gga gcc gtt caa aat	1824		
180	Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn			
181		595	600	605
184	gag atc acc ctc aca cat ccc ata acc aaa ttc gtc atg gca tgc atg	1872		
185	Glu Ile Thr Leu Thr His Pro Ile Thr Lys Phe Val Met Ala Cys Met			
186		610	615	620
188	tcg gcc gac ctg gag gtc gtc act agc acc tgg gtg ctg gta ggc gga	1920		
189	Ser Ala Asp Leu Glu Val Val Thr Ser Thr Trp Val Leu Val Gly Gly			
190	625	630	635	640

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Input Set : A:\pto.da.txt

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192	gtc	ctt	gca	gct	ctg	gcc	gca	tat	tgc	ctg	aca	acc	ggt	agt	gtg	gtc	1968
193	Val	Leu	Ala	Ala	Leu	Ala	Ala	Tyr	Cys	Leu	Thr	Thr	Gly	Ser	Val	Val	
194					645					650					655		
196	att	gtg	ggt	agg	atc	att	ttg	tcc	ggg	agg	ccg	gct	ggt	ggt	ccc	gac	2016
197	Ile	Val	Gly	Arg	Ile	Ile	Leu	Ser	Gly	Arg	Pro	Ala	Val	Val	Pro	Asp	
198				660					665					670			
200	agg	gaa	gtc	ctc	tac	cgg	gag	ttc	gat	gaa	atg	gaa	gag	tgc	gcc	tca	2064
201	Arg	Glu	Val	Leu	Tyr	Arg	Glu	Phe	Asp	Glu	Met	Glu	Glu	Cys	Ala	Ser	
202			675					680					685				
204	cac	ctc	cct	tac	atc	gag	caa	gga	atg	cag	ctc	gcc	gag	cag	ttc	aag	2112
205	His	Leu	Pro	Tyr	Ile	Glu	Gln	Gly	Met	Gln	Leu	Ala	Glu	Gln	Phe	Lys	
206		690					695				700						
208	cag	cag	gca	ctc	ggg	ttg	ctg	caa	aca	gcc	acc	aag	caa	gcg	gag	gcc	2160
209	Gln	Gln	Ala	Leu	Gly	Leu	Leu	Gln	Thr	Ala	Thr	Lys	Gln	Ala	Glu	Ala	
210	705				710					715					720		
212	gct	gct	ccc	gtg	gtg	gag	tcc	agg	tgg	cgg	gcc	ctt	gag	gcc	ttc	tgg	2208
213	Ala	Ala	Pro	Val	Val	Glu	Ser	Arg	Trp	Arg	Ala	Leu	Glu	Ala	Phe	Trp	
214				725					730					735			
216	gca	aag	cac	atg	tgg	aac	ttc	atc	agc	ggg	ata	cag	tac	tta	gca	ggc	2256
217	Ala	Lys	His	Met	Trp	Asn	Phe	Ile	Ser	Gly	Ile	Gln	Tyr	Leu	Ala	Gly	
218			740					745					750				
220	tta	tcc	act	ctg	cct	ggg	aac	ccc	gcg	ata	gca	tca	ctg	atg	gca	ttc	2304
221	Leu	Ser	Thr	Leu	Pro	Gly	Asn	Pro	Ala	Ile	Ala	Ser	Leu	Met	Ala	Phe	
222			755				760					765					
224	aca	gcc	tct	atc	acc	agt	ccg	ctc	acc	acc	cag	aat	acc	ctc	cta	ttc	2352
225	Thr	Ala	Ser	Ile	Thr	Ser	Pro	Leu	Thr	Thr	Gln	Asn	Thr	Leu	Leu	Phe	
226		770					775					780					
228	aac	atc	tta	ggg	gga	tgg	gtg	gct	gct	caa	ctc	gct	cct	ccc	agt	gct	2400
229	Asn	Ile	Leu	Gly	Gly	Trp	Val	Ala	Ala	Gln	Leu	Ala	Pro	Pro	Ser	Ala	
230	785				790					795					800		
232	gct	tcg	gcc	ttc	gtg	ggt	gcc	ggc	att	gcc	ggt	gcg	gcc	att	ggc	agc	2448
233	Ala	Ser	Ala	Phe	Val	Gly	Ala	Gly	Ile	Ala	Gly	Ala	Ala	Ile	Gly	Ser	
234				805					810					815			
236	ata	ggc	ctt	ggg	aag	gtg	ctt	gtg	gac	att	ctg	gcg	ggc	tat	gga	gcg	2496
237	Ile	Gly	Leu	Gly	Lys	Val	Leu	Val	Asp	Ile	Leu	Ala	Gly	Tyr	Gly	Ala	
238			820					825					830				
240	ggg	gtg	gcc	ggt	gca	ctc	gtg	gct	ttt	aag	gtc	atg	agc	ggc	gag	gcg	2544
241	Gly	Val	Ala	Gly	Ala	Leu	Val	Ala	Phe	Lys	Val	Met	Ser	Gly	Glu	Ala	
242			835					840					845				
245	ccc	tcc	gcc	gag	gac	ctg	gtt	aac	ttg	ctc	cct	gcc	atc	ctc	tcc	ccc	2592
246	Pro	Ser	Ala	Glu	Asp	Leu	Val	Asn	Leu	Leu	Pro	Ala	Ile	Leu	Ser	Pro	
247		850					855					860					
249	ggc	gcc	ttg	gtc	gtc	ggg	atc	gtg	tgt	gca	gca	atc	ctg	cgt	cgg	cac	2640
250	Gly	Ala	Leu	Val	Val	Gly	Ile	Val	Cys	Ala	Ala	Ile	Leu	Arg	Arg	His	
251	865				870					875				880			
253	gtg	ggc	ccg	gga	gag	ggg	gct	gtg	cag	tgg	atg	aac	cgg	ctg	ata	gcg	2688
254	Val	Gly	Pro	Gly	Glu	Gly	Ala	Val	Gln	Trp	Met	Asn	Arg	Leu	Ile	Ala	
255				885					890					895			
257	ttc	gct	tcg	cgg	ggt	aac	cac	gtt	tcc	ccc	acg	cac	tac	gtg	cct	gag	2736

RAW SEQUENCE LISTING

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Input Set : A:\pto.da.txt

Output Set: N:\CRF4\12202005\J559431.raw

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258 Phe Ala Ser Arg Gly Asn His Val Ser Pro Thr His Tyr Val Pro Glu
259          900          905          910
261 agc gac gcc gca gca cgt gta act cag atc ctc tcc agc ctc acc atc      2784
262 Ser Asp Ala Ala Ala Arg Val Thr Gln Ile Leu Ser Ser Leu Thr Ile
263          915          920          925
265 act cag ctg ctg aag agg ctt cac cag tgg att aat gag gac tgc tcc      2832
266 Thr Gln Leu Leu Lys Arg Leu His Gln Trp Ile Asn Glu Asp Cys Ser
267          930          935          940
269 acg cca tgc taa      2844
270 Thr Pro Cys
271 945
274 <210> SEQ ID NO: 2
275 <211> LENGTH: 947
276 <212> TYPE: PRT
277 <213> ORGANISM: Artificial sequence
279 <220> FEATURE:
280 <223> OTHER INFORMATION: sequence coding for NS3NS4
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288          20          25          30
290 Glu Val Gln Val Leu Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys
291          35          40          45
293 Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr
294          50          55          60
296 Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp
297 65          70          75          80
299 Gln Asp Leu Val Gly Trp Pro Ala Pro Pro Gly Ala Arg Ser Met Thr
300          85          90          95
302 Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala
303          100         105         110
306 Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu
307          115         120         125
309 Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu
310          130         135         140
312 Leu Cys Pro Ser Gly His Val Val Gly Ile Phe Arg Ala Ala Val Cys
313 145         150         155         160
315 Thr Arg Gly Val Ala Lys Ala Val Asp Phe Ile Pro Val Glu Ser Met
316          165         170         175
318 Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro
319          180         185         190
321 Ala Val Pro Gln Thr Phe Gln Val Ala His Leu His Ala Pro Thr Gly
322          195         200         205
324 Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr
325          210         215         220
327 Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly
329 225         230         235         240
331 Ala Tyr Met Ser Lys Ala His Gly Ile Glu Pro Asn Ile Arg Thr Gly

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VERIFICATION SUMMARY

DATE: 12/20/2005

PATENT APPLICATION: US/10/559,431

TIME: 13:16:58

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\12202005\J559431.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:30 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:28
L:481 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:479
L:771 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:769
L:997 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:995

Raw Sequence Listing before editing,
for reference only



IFWP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/559,431

DATE: 12/16/2005

TIME: 15:37:52

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4 <110> APPLICANT: BIOMERIEUX
 5 INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
 7 <120> TITLE OF INVENTION: Composition comprising the polyprotein NS3/NS4 and the
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 8 of HCV, expression vectors including the corresponding nucleic sequences and
 9 their therapeutic use
 11 <130> FILE REFERENCE: ADENOVIR
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/559,431
 C--> 13 <141> CURRENT FILING DATE: 2005-12-05
 13 <160> NUMBER OF SEQ ID NOS: 27
 15 <170> SOFTWARE: PatentIn version 3.1

Does Not Comply
 Corrected Diskette Needed

(pg-1)

ERRORED SEQUENCES

1565 <210> SEQ ID NO: 27
 1566 <211> LENGTH: 9
 1567 <212> TYPE: PRT
 1568 <213> ORGANISM: Artificial sequence
 1570 <220> FEATURE:
 1571 <223> OTHER INFORMATION: epitope DLM
 1573 <400> SEQUENCE: 27
 1575 Asp Leu Met Gly Tyr Ile Pro Leu Val
 1576 1 5
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 E--> 1581 ??
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VERIFICATION SUMMARY

DATE: 12/16/2005

PATENT APPLICATION: US/10/559,431

TIME: 15:37:54

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\12162005\J559431.raw

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L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:30 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:28
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L:771 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:769
L:997 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:995
L:1579 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:1579 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
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L:1585 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:1585 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:1590 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:27